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=> d his

     (FILE 'HOME' ENTERED AT 13:27:09 ON 09 MAY 2001)

     FILE 'REGISTRY' ENTERED AT 13:27:19 ON 09 MAY 2001
L1              1 S 61116-22-1/RN

     FILE 'CAPLUS' ENTERED AT 13:28:29 ON 09 MAY 2001

     FILE 'REGISTRY' ENTERED AT 13:28:36 ON 09 MAY 2001
                  SET SMARTSELECT ON
L2            SEL L1 1- CHEM :       8 TERMS
                  SET SMARTSELECT OFF

     FILE 'CAPLUS' ENTERED AT 13:28:37 ON 09 MAY 2001
L3           1016 S L2
                  E DICARBOXYLIC ACID/CT
                  E DICARBOXYLIC ACIDS/CT
                  E E3 + ALL
                  E MONOCARBOXYLIC ACIDS/CT
                  E E3 + ALL
                  E CARBOXYLIC ACIDS/CT
L4            425 S CANDIDA MALTOSA OR CANDIDA CLOACAE OR CANDIDA NOVELLUS OR
CAN
L5              7 S L3 (L) L4
L6              7 DUP REM L5 (0 DUPLICATES REMOVED)
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=> s 61116-22-1/rn
L1            1 61116-22-1/RN

=> d

L1    ANSWER 1 OF 1  REGISTRY  COPYRIGHT 2001 ACS
RN    61116-22-1  REGISTRY
CN    Oxidase, acyl coenzyme A (9CI)  (CA INDEX NAME)
OTHER NAMES:
CN    Acyl coenzyme A oxidase
CN    Acyl-CoA oxidase
CN    E.C. 1.3.3.6
CN    Fatty acyl-CoA oxidase
CN    Fatty acyl-coenzyme A oxidase
CN    Long-chain acyl-CoA oxidase
CN    Medium-chain acyl-CoA oxidase
MF    Unspecified
CI    MAN
LC    STN Files:   AGRICOLA, ANABSTR, BIOBUSINESS, BIOSIS, BIOTECHNO, CA,
        CAPLUS, CHEMCATS, CSCHEM, EMBASE, MSDS-OHS, PROMT, TOXLIT, USPATFULL

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
             772 REFERENCES IN FILE CA (1967 TO DATE)
               1 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA
             774 REFERENCES IN FILE CAPLUS (1967 TO DATE)
```

=> d ibib ab hit 1-7

L6   ANSWER 1 OF 7 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1998:6010 CAPLUS
DOCUMENT NUMBER: 128:125658
TITLE: Effect of cultivation conditions on the level of enzymes of n-alkane metabolism in Candida maltosa cells
AUTHOR(S): Sharyshev, A. A.; Peskova, E. V.; Komarova, G. N.
CORPORATE SOURCE: Institute of Biochemistry and Physiology of Microorganisms, Russian Academy of Sciences, Pushchino, 142292, Russia
SOURCE: Microbiology (Moscow)(Transl. of Mikrobiologiya) (1997), 66(6), 652-656
CODEN: MIBLAO; ISSN: 0026-2617
PUBLISHER: MAIK Nauka/Interperiodica Publishing
DOCUMENT TYPE: Journal
LANGUAGE: English
AB   The effect of cultivation conditions on the content of cytochromes and the activities of the key enzymes of n-alkane metab. was studied in the yeast Candida maltosa. Stationary-phase cells, grown on various substrates, were found to exhibit similar levels of cytochromes and enzymes.
IT   544-76-3, Hexadecane   9001-16-5   9007-43-6, Cytochrome c, biological studies   9035-37-4, Cytochrome b   9035-51-2, Cytochrome P 450, biological studies   9045-78-7, Isocitrate lyase   9073-63-6, Alcohol oxidase **61116-22-1, Acyl-CoA oxidase**
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(effect of cultivation conditions on level of enzymes of n-alkane metab. in **Candida maltosa** cells)

L6   ANSWER 2 OF 7 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1995:706945 CAPLUS
DOCUMENT NUMBER: 123:106044
TITLE: Fatty acid oxidation enzymes of the yeast Candida cloacae
AUTHOR(S): West, Mark A.; Hill, Judy; Watson, Martin; Simon, William; Lindner, Nigel; Casey, John; Slabas, Antoni R.
CORPORATE SOURCE: Department Biological Sciences, University Durham, Durham, DH1 3LE, UK
SOURCE: Plant Lipid Metab., [Pap. Int. Meet. Plant Lipids], 11th (1995), Meeting Date 1994, 268-70. Editor(s): Kader, Jean-Claude; Mazliak, Paul. Kluwer: Dordrecht, Neth.
CODEN: 61OZAO
DOCUMENT TYPE: Conference
LANGUAGE: English
AB   Cultures of parent and mutant strains of C. cloacae were grown under lab. conditions, and their induction patterns were compared over time for several enzymes of fatty acid oxidn. Alc. oxidase, an enzyme in the .omega.-oxidn. pathway, was purified 35-fold. The protein had a Mr of 70,000 and oxidized long-chain fatty alcs.
IT   9074-19-5, Hydratase **61116-22-1, Acyl-CoA oxidase**
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
(induction and purifn. of fatty acid oxidn. enzymes of **Candida cloacae**)

L6 ANSWER 3 OF 7 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1996:58714 CAPLUS
DOCUMENT NUMBER: 124:166891
TITLE: Cloning and characterization of the POX2 gene in Candida maltosa
AUTHOR(S): Masuda, Yutaka; Park, Sun Mee; Ohta, Akinori; Takagi, Masamichi
CORPORATE SOURCE: Tokyo, 113, Japan
SOURCE: Gene (1995), 167(1/2), 157-61
CODEN: GENED6; ISSN: 0378-1119
DOCUMENT TYPE: Journal
LANGUAGE: English

AB To study the function of **acyl-CoA oxidase** in an n-alkane-assimilating yeast, **Candida maltosa**, the authors isolated the POX2 gene which is a member of the **acyl-CoA oxidase** gene family. POX2 had a 2172-bp open reading frame (ORF) encoding an approx. 84-kDa polypeptide (724 amino acids (aa)) and was contiguous to POX4, another member of the **acyl -CoA oxidase** gene family on the same chromosomal DNA in a convergent arrangement. Northern blot anal. revealed that the expression of POX2 was induced in cells grown on oleic acid, n-tetradecanol and n-tetradecane. By using a gene-disruption technique, the authors constructed strains (termed P2DD and P4DD) in which both alleles of POX2 and POX4 were disrupted. The P2DD strain was normal in assimilation of various hydrophobic carbon sources, such as n-tetradecane, n-tetradecanol and oleic acid. In contrast, the P4DD strain was defective in its ability to grow on such hydrophobic carbon sources.

AB To study the function of **acyl-CoA oxidase** in an n-alkane-assimilating yeast, **Candida maltosa**, the authors isolated the POX2 gene which is a member of the **acyl-CoA oxidase** gene family. POX2 had a 2172-bp open reading frame (ORF) encoding an approx. 84-kDa polypeptide (724 amino acids (aa)) and was contiguous to POX4, another member of the **acyl -CoA oxidase** gene family on the same chromosomal DNA in a convergent arrangement. Northern blot anal. revealed that the expression of POX2 was induced in cells grown on oleic acid, n-tetradecanol and n-tetradecane. By using a gene-disruption technique, the authors constructed strains (termed P2DD and P4DD) in which both alleles of POX2 and POX4 were disrupted. The P2DD strain was normal in assimilation of various hydrophobic carbon sources, such as n-tetradecane, n-tetradecanol and oleic acid. In contrast, the P4DD strain was defective in its ability to grow on such hydrophobic carbon sources.

ST sequence gene POX2 **Candida maltosa; acyl CoA oxidase** gene sequence Candida

IT **61116-22-1**, Oxidase, acyl coenzyme A
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(cloning, characterization and sequence of the POX2 gene in **Candida maltosa**)

L6 ANSWER 4 OF 7 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1989:167156 CAPLUS
DOCUMENT NUMBER: 110:167156
TITLE: Expression and transport of Candida tropicalis peroxisomal **acyl-coenzyme**

A oxidase in the yeast
Candida maltosa

AUTHOR(S): Kamiryo, Tatsuyuki; Sakasegawa, Yuji; Tan, Hironobu
CORPORATE SOURCE: Fac. Integr. Arts Sci., Hiroshima Univ., Hiroshima, 730, Japan
SOURCE: Agric. Biol. Chem. (1989), 53(1), 179-86
CODEN: ABCHA6; ISSN: 0002-1369
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The genes POX2 and POX4, which encode the subunits (PXP-2 and PXP-4) of peroxisomal fatty acyl-CoA oxidase of C. tropicalis, were introduced into the related yeast C. maltosa. The cells transformed with POX2 or POX4 showed high level expression of PXP-2 or PXP-4 in the purified peroxisomes. The polypeptides assocd. with the heterologous organelle were resistant to added protease, implying that they were transported into the peroxisomes. Truncated genes for PXP-4 were constructed in vitro and introduced into the host cells. Peptide-C, the COOH-terminal two-thirds of PXP-4, was efficiently transported into the host peroxisomes, and the polypeptide contg. the NH2-terminal one-third was also, in much lesser amt. These and other results suggested that there were at least 2 regions of peroxisomal targeting information in PXP-4 and the primary information was internal. Deletions in Peptide-C inhibited the transported of many, but not all, of the host-cell peroxisomal polypeptides. This suggested the existence of heterogeneous transport systems on the peroxisomal membrane.

TI Expression and transport of Candida tropicalis peroxisomal **acyl-coenzyme A oxidase** in the yeast **Candida maltosa**

IT **Candida maltosa**
(expression and transport of Candida tropicalis **fatty acyl-CoA oxidase** subunits in)

IT Candida tropicalis
(**fatty acyl-CoA oxidase** of peroxisome of, expression and transport in **Candida maltosa** of subunits of)

IT Peroxisome
(**fatty acyl-CoA oxidase** subunits of, of Candida tropicalis, expression and transport in **Candida maltosa** of)

IT Biological transport
(of **fatty acyl-CoA oxidase** of Candida tropicalis, into **Candida maltosa** peroxisomes, peroxisomal targeting sequences in relation to)

IT Molecular cloning
(of Candida tropicalis peroxisomal **fatty acyl-CoA oxidase** subunit genes, in **Candida maltosa**, peroxisomal transport in relation to)

IT Gene and Genetic element, microbial
RL: BIOL (Biological study)
(POX2, for **fatty acyl-CoA oxidase** subunit, of Candida tropicalis peroxisome, expression in **Candida maltosa** of)

IT Gene and Genetic element, microbial
RL: BIOL (Biological study)
(POX4, for **fatty acyl-CoA oxidase** subunit, of Candida tropicalis peroxisome, expression in **Candida maltosa** of)

IT **61116-22-1, Fatty acyl-coenzyme**

A oxidase
RL: PRP (Properties)
(of Candida tropicalis peroxisome, expression and transport in **Candida maltosa** of subunits of)

L6 ANSWER 5 OF 7 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 1988:449343 CAPLUS
DOCUMENT NUMBER: 109:49343
TITLE: Complete nucleotide sequence of the peroxisomal **acyl CoA oxidase** from the alkane-utilizing yeast **Candida maltosa**
AUTHOR(S): Hill, David E.; Boulay, Richard; Rogers, David
CORPORATE SOURCE: Genet. Inst., Cambridge, MA, 02140, USA
SOURCE: Nucleic Acids Res. (1988), 16(1), 365-6
CODEN: NARHAD; ISSN: 0305-1048
DOCUMENT TYPE: Journal
LANGUAGE: English

AB A 2127-nucleotide open reading frame of C. maltosa which codes for a 709-amino acid acyl CoA oxidase (AOX) was sequenced. The gene is 81% similar to the AOX gene of C. tropicalis.

TI Complete nucleotide sequence of the peroxisomal **acyl CoA oxidase** from the alkane-utilizing yeast **Candida maltosa**

IT **Candida maltosa**
(**acyl CoA oxidase** gene of, nucleotide and encoded peptide sequences of)

IT Peroxisome
(**acyl CoA oxidase** of, of **Candida maltosa**, gene for, nucleotide and encoded peptide sequences)

IT Gene and Genetic element, microbial
RL: BIOL (Biological study)
(for **acyl CoA oxidase**, of **Candida maltosa**, nucleotide and encoded peptide sequences of)

IT Protein sequences
(of **acyl CoA oxidase**, of **Candida maltosa**, complete)

IT Deoxyribonucleic acid sequences
(**acyl CoA oxidase**-specifying, of **Candida maltosa**, complete)

IT **61116-22-1, Acyl CoA oxidase**
RL: PRP (Properties)
(gene for, of **Candida maltosa**, nucleotide and encoded peptide sequences of)

L6 ANSWER 6 OF 7 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 1981:170259 CAPLUS
DOCUMENT NUMBER: 94:170259
TITLE: Purification of acylcoenzyme A oxidase
PATENT ASSIGNEE(S): Amano Pharmaceutical Co., Ltd., Japan
SOURCE: Jpn. Kokai Tokkyo Koho, 8 pp.
CODEN: JKXXAF
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
JP 56008684	A2	19810129	JP 1979-81324	19790629

JP 60013664 B4 19850409

AB **Acyl-CoA oxidase** (I) is purified by adsorption on a water-insol. carrier contg. CH3(CH2)n or NH2(CH2)m groups, where n = 1-3 and m = 2-8. Thus, an enzyme soln. prepd. from a culture of **Candida maltosa** IAM 12247 was dialyzed against 50 mM phosphate buffer (pH 8.0) and charged to a column of CH3(CH2)3-Sepharose buffered to pH 8.0 with the phosphate buffer. The column was washed with the phosphate buffer contg. 0.1M NaCl and enzyme was eluted with the buffer contg. 0.5M NaCl. The eluate was mixed with (NH4)2SO4 at 80% satn. and the resulting ppt. was dialyzed and lyophilized to yield purified I (11.3 units/mg) free from catalase, other oxidases, lipase, and esterase.

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IT **Candida maltosa**
(**acyl CoA oxidase** of)

IT **61116-22-1P**
RL: PREP (Preparation)
(of **Candida maltosa**, purifn. and properties of)

L6 ANSWER 7 OF 7 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 1981:190327 CAPLUS
DOCUMENT NUMBER: 94:190327
TITLE: Acyl coenzyme A oxidase
PATENT ASSIGNEE(S): Amano Pharmaceutical Co., Ltd., Japan
SOURCE: Jpn. Kokai Tokkyo Koho, 6 pp.
CODEN: JKXXAF
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
JP 56008683	A2	19810129	JP 1979-81323	19790629

AB Acyl CoA oxidase (I) [61116-22-1] is produced by culturing yeast (esp. Candida), fungi, or Streptomyces. Thus, C. maltosa IAM 12247 was cultured with shaking at 30.degree. for 24 h on a medium (pH 5.2) contg. n-alkane mixt. 1, (NH4)H2PO4 0.5, KH2PO4 0.25, MgSO4 0.1, and yeast ext. 0.25%. The cells (22 g) were suspended in 50 mM phosphate buffer (pH 7.2) and disintegrated with a Dyno mill. The homogenate was mixed with (NH4)2SO4 at 45% satn. and centrifuged. The resulting ppt. was extd. with 50 mM phosphate buffer (pH 7.2) contg. 0.5% Triton X-100. The ext. was subjected to column chromatog. on Sephadex G-25 and DEAE-cellulose to yield 150 mg yellow powd. I.

IT **Candida maltosa**

(**acyl CoA oxidase** prodn. with)

IT Fermentation

(**acyl CoA oxidase**, with **Candida maltosa**)

IT **61116-22-1P**

RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)

(manuf. of, with **Candida maltosa**)

L2 ANSWER 1 OF 1 REGISTRY COPYRIGHT 2001 ACS
RN **9023-03-4** REGISTRY
CN Reductase, cytochrome c (reduced nicotinamide adenine dinucleotide phosphate) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN Cytochrome c reductase
CN Cytochrome c reductase (NADPH)
CN Cytochrome c reductase (NADPH-dependent)
CN Cytochrome c reductase (reduced nicotinamide adenine dinucleotide phosphate)
CN Dihydronicotinamide adenine dinucleotide phosphate-cytochrome c reductase
CN E.C. 1.6.2.4
CN FAD-cytochrome c reductase
CN NADP-cytochrome c reductase
CN NADPH-cytochrome c oxidoreductase
CN NADPH-cytochrome c reductase
CN NADPH-dependent cytochrome c reductase
CN NADPH-ferricytochrome c oxidoreductase
CN NADPH-ferrihemoprotein reductase
CN Reduced nicotinamide adenine dinucleotide phosphate-cytochrome c reductase
CN TPNH-cytochrome c reductase
MF Unspecified
CI MAN
LC STN Files: AGRICOLA, BIOBUSINESS, BIOSIS, BIOTECHNO, CA, CAPLUS, EMBASE, PIRA, PROMT, TOXLINE, TOXLIT, ULIDAT, USPATFULL

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
2887 REFERENCES IN FILE CA (1967 TO DATE)
3 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA
2887 REFERENCES IN FILE CAPLUS (1967 TO DATE)

NiceZyme View of ENZYME: EC 1.6.2.4

Official Name

NADPH--ferrihemoprotein reductase.

Alternative Name(s)

NADPH--cytochrome p450 reductase.
TPNH(2) cytochrome c reductase.
Ferrihemoprotein p450 reductase.

Reaction catalysed

```
    NADPH
 +  2 ferricytochrome
<=>
    NADP(+)
 +  2 ferrocytochrome
```

Cofactor(s)

FMN; FAD.

Comments

- Catalyses the reduction of heme-thiolate-dependent monooxygenases such as EC 1.14.14.1, and is part of the microsomal hydroxylating system.
- Also reduces cytochrome b5 and cytochrome c.

Cross-References

Biochemical Pathways; map number(s)	T6, U6
BRENDA	1.6.2.4
EMP/PUMA	1.6.2.4
WIT	1.6.2.4
KYOTO UNIVERSITY LIGAND CHEMICAL DATABASE	1.6.2.4
MEDLINE	Find literature relating to 1.6.2.4
SWISS-PROT	P14779, CPXB_BACME; P50126, NCPR_CANMA; P37201, NCPR_CANTR; Q05001, NCPR_CATRO; P37039, NCPR_CAVPO; P16435, NCPR_HUMAN; P37040, NCPR_MOUSE; Q07994, NCPR_MUSDO; P37116, NCPR_PHAAU; [illegible]

	P19618, NCPR_SALTR; P36587, NCPR_SCHPO; P16603, NCPR_YEAST;

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BRENDA:1.6.2.4

E.C. number	1.6.2.4 (BRENDA copyright notice)
Original Organism	#1# Pig <1, 11, 14, 15, 29, 32, 35, 38, 47> #2# Rat <2, 5, 10, 16, 27, 29, 31, 33, 34, 36, 41, 43, 46> #3# Rabbit <3, 4, 30, 39> #4# Human <45> #5# Helianthus tuberosus (L. var. Blanc commun., Jerusalem artichoke) <6, 9> #6# Nitrobacter winogradskyi <7> #7# Hamster <8> #8# Trypanosoma cruzi <12> #9# Trichosporon cutaneum <13> #10# Lodderomyces elongisporus <17> #11# Aspergillus ochraceus <18> #12# Saccharomyces cerevisiae (grown anaerobically) <19, 23, 28, 37, 42> #13# Candida tropicalis (grown on alkanes) <20, 22, 26> #14# Spodoptera eridania (southern Armyworm) <21> #15# Catharanthus roseus <24> #16# Tetrahymena pyriformis <40> #17# Plants (e.g. maize, potato, avocado, bramble, tulip, leek, Vicia faba, sunflower) <6> #18# Housefly <44> #19# Horse <5> #20# Chicken <25>
Systematic name	NADPH:ferrihemoprotein oxidoreductase
Recommended name	NADPH-ferrihemoprotein reductase

Synonyms	Dihydroxynicotinamide adenine dinucleotide phosphate-cytochrome c reductase EC 1.6.99.2 #2# (formerly) <27> Aldehyde reductase (NADPH-dependent) #2# <10> NADPH-cytochrome p-450 reductase #2# <10, 27> FAD-cytochrome c reductase NADP-cytochrome c reductase NADPH-dependent cytochrome c reductase NADPH-ferricytochrome c oxidoreductase NADPH-cytochrome c oxidoreductase Reduced nicotinamide adenine dinucleotide phosphate-cytochrome c reductase TPNH-cytochrome c reductase NADPH-cytochrome c reductase Reductase, cytochrome c (reduced nicotinamide adenine dinucleotide phosphate) Ferrihemprotein P450 reductase TPNH2 cytochrome c reductase NADP-cytochrome reductase Cytochrome c reductase (reduced nicotinamide adenine dinucleotide phosphate, NADPH, NADPH-dependent)
CAS registration number	9023-03-4
Reaction	NADPH + 2 ferricytochrome = NADP+ + 2 ferrocytochrome
Reaction type	Redox reaction

Substrates/products	S: NADPH + O2 #1,12# (slow reaction, presence of menadione, or duroquinone, or vitamin K3 essential) <14, 28> P: NADP+ + O2- #1,12# (superoxide anion) <14, 28> S: More #1-3# (O-deethylation of 7-ethoxycoumarin, #3# <30>; N-demethylation of benzphetamine, #2,3# <30, 33>; aniline hydroxylase, #2# <33>; as part of MEOS i.e. microsomal ethanol-oxidizing system composed of NADPH-cytochrome c reductase, Cytochrome P-450, phospholipids, #2# <33>; omega-hydroxylation of fatty acids together with cytochrome P-450, #1# <38>) <30, 33, 38> P: ? S: 17-Hydroxyprogesterone + NADPH #2# <34> P: Androstendione + 2-carbon fragment #2# (removal of 2-carbon side chain from 17-position of 21-carbon steroids) <34> S: NADPH + cinnamate #5# <9> P: NADP+ + p-coumarate #5# <9> S: NADPH + ferricytochrome c #1-3,5-8,10,12-15,19# (NADH less than 5% of NADPH activity, #1# <1>; additional electron acceptors: 2,6-dichlorophenolindophenol, #1,2,5,6,8,10,12-15# <6, 7, 12, 14, 17, 20, 21, 24, 26, 28, 36>; cytochrome P-450, #1,2,5,7,13# <1, 8, 9, 20, 36, 38>; ferricyanide, #5,8,10,12-15# <6, 9, 12, 17, 20, 21, 24, 26, 28>; menadione, #6,8,13# <7, 12, 20, 26>; neotetrazolium chloride, #2,13# <20, 26, 36>; nitroblue tetrazolium salt, #1# <14>; vitamin K3, #2# <36>; benzoquinone, #2# <36>) <1, 4-9, 12, 14, 17, 20, 21, 24, 26, 28, 36, 38> P: NADP+ + ferrocytochrome c S: NADPH + hexadecanal #2# (hexadecanol replaceable by p-nitroacetophenone, or p-pyridinecarboxaldehyde, or p-nitrobenzaldehyde) <10> P: NADP+ + hexadecanol #2# <10>
Natural substrates	More #2,3,13# (monooxygenase system composed of cytochrome P-450, NADPH-cytochrome c reductase, phospholipids, #2,13# <16, 26>; detoxification of drugs, inactivation of procarcinogens, #2# <16>; biotransformation of airborne compounds, #3# <30>) <16, 26, 30> NADPH + cytochrome P-450 #5,17# <6>
Turnover number (1/min)	6100 #13# {cytochrome c} <26> 3870 #8# {ferricyanide} <12> 897 #8# {cytochrome c} <12> 458 #8# {2,6-dichlorophenolindophenol} <12> 87 #8# {menadione} <12> -999 #1,2# <29, 31, 33>

Specific activity (micromol/min/mg)	150-180 #12# <28> 63.8 #2# <16> 40 #19# <5> 15.2 #1# <1> -999 #1-3,5-7,9,13,15,20# <3, 7, 8-11, 13, 14, 20, 24, 25, 27, 30, 34, 36>
Km-value (mM)	7.2 #2# {ethanol} (microsomal ethanol oxidizing system) <33> 2.5 #2# {benzalacetone} <10> 1.4 #2# {p-nitroacetophenone} <10> 0.31 #2# {p-nitrobenzaldehyde} <10> 0.077 #13# {2,6-dichlorophenolindophenol} <26> 0.03 #2# {hexadecanol} <10> 0.022 #1# {NADPH} (similar values, #1,5,12,14# <9, 14, 21, 28>) <11> 0.013 #2,14# {cytochrome c} (similar value, #1# <32>) <5, 21> 0.0082 #19# {cytochrome c} <5> 0.006 #1# {cytochrome c} (similar values, #5# <9>) <35> 0.0053 #1# {menadione} <14> 0.0036 #1# {NADPH} (similar values, #1,3,6,8,14,15,20# <4, 7, 12, 21, 24, 25, 32, 35>) <1> 0.0019 #3# {azidonitrophenyl-gamma-aminobutyryl-NADPH} <4> -999 #1,8# (O2-generation, #1# <14>) <11, 12, 14>
pH-optimum	8-9 #1# <35> 7.8 #13# <20> 7.8-8 #12,20# <25, 28> 7.7 #11# <18> 7.5-9 #14# <21> 7-7.4 #1# (O2- generation) <14> 6.9-7.5 #2# (microsomal ethanol-oxidizing system) <33>
pH-range	7-8.5 #13# (less than 50% of maximal activity above and below) <26> 6.5-9 #14# <21>

Cofactors/prosthetic groups	FAD #1-3,5-8,10,12-15,20# (ratio FAD:FMN 1:1, #1,5,10,12-14# <1, 9, 11, 17, 20, 21, 26, 28>; 1 mol per subunit, #6,8,12# <7, 12, 23>; tightly bound, #12,13# <20, 28>; loosely bound, #12# <42>) <1-3, 7-9, 11, 12, 17, 20, 21, 23-26, 28, 31-33, 35, 42> FMN #1-3,5,7,10,12-15,20# (ratio FAD:FMN 1:1, #1,5,10,12-14# <1, 9, 11, 17, 20, 21, 26, 28>; tightly bound, #13# <20>; loosely bound, #12# <28, 42>; 1 mol per mol of enzyme, #10,13# <17, 20>) <1-3, 8, 9, 11, 17, 20, 21, 23-26, 28, 31, 32, 35, 42> Menadione #14# (slight stimulation) <21> NADPH #1-3,5-8,10,12-15,17,19# (NADH less than 5% of NADPH activity, #1# <1>; not replaceable by NADH, #2# <33>) <1, 4-9, 12, 14, 17, 20, 21, 24, 28, 33, 36, 38> Nonionic detergent #10# (activation) <17>
Metal ions/salts	More #5,15# (stimulation by increasing ionic strength) <9, 24>
Inhibitors	2'-AMP #14# <21> 2,6-Dichlorophenol-indophenol #1# (formation of superoxide anion) <14> 3-Aminonicotinamide adenine dinucleotide phosphate #5# <6> 5,5'-Dithiobis(2-nitrobenzoate) #12# (in absence of FAD or NADPH) <23> Alizarin #14# <21> CO #2# <33> HgCl2 #12,13# <20, 26, 28> High ionic strength #5# <9> Mersalyl #3,14# <3, 21> N2 #2# <33> NAD+ #6# <7> NADP+ #1,5,6,13,14# <6, 7, 9, 21, 26, 32> p-Chloromercuribenzoate #12-15# <20, 21, 24, 26, 28> Sodium formate #2# <33>

Source tissue	Brain #2# <10> Bulbs #17# (tulip) <6> Cell #6# <7> Endometrium #1# <15> Epimastigotes #8# <12> Kidney #1,20# <25, 32, 35> Liver #1-3,7# <2, 5, 8, 16, 27, 29, 31, 33, 34, 36, 38, 39, 43, 46, 47> Lung #3# <30> Mesocarp #17# (avocado) <6> Midgut #14# (of larvae) <21> Peritoneal neutrophils #3# <3> Placenta #4,19# <5, 45> Polymorphonuclear leukocytes #1# <1, 14> Seedlings #15,17# (Vicia faba, leek, sunflower, #17# <6>) <6, 24> Spleen #1# <35> Testis #1# <11> Tuber #5# <6, 9>
Localisation	Cytosol #6,8# <7, 12> Endoplasmic reticulum #2# <43> membrane-bound #1,3,13,20# (outer membrane of mitochondria, #20# <25>) <1, 3, 4, 14, 20, 25> Microsomes #1,2,5,7,9-12,14,16,19# <2, 5, 8-10, 13, 15-18, 21, 31, 33, 35-38, 40> Nuclear envelope #2# <27> Nucleus #12# (low activity) <19> Spheroplasts #12# <19>

Purification	#1# <1, 11, 14, 29, 38, 47> #10# <17> #12# <23, 28> #13# <20, 26> #14# <21> #15# <24> #19# <5> #2# (FAD-depleted enzyme <2>) <2, 5, 10, 16, 29, 33, 36, 41> #3# <3, 30> #5# <9> #6# <7> #7# <8> #8# <12>
Crystallisation	#12# (Saccharomyces cerevisiae) <23>
Molecular Weight	400000 #1# (pig, gel filtration) <1> 100000 #8# (Trypanosoma cruzi, gel filtration) <12> 82000-85000 #4,5,12,18# (Helianthus tuberosus, SDS-PAGE followed by Western blotting <6>; Saccharomyces cerevisiae, calculation from FAD content <28>; house fly <44>; human placenta <45>) <6, 28, 44, 45> 78000-79000 #2,3# (rabbit, sedimentation equilibrium centrifugation <39>; rat liver <46>) <39, 46> 70000 #1,6,12# (Nitrobacter winogradskyi, gel filtration <7>; pig testis, gel filtration <11>; Saccharomyces cerevisiae, gel filtration <28>) <7, 11, 28> 65000-68000 #1,3,12,13# (Saccharomyces cerevisiae, sedimentation equilibrium centrifugation, values depending on pH <23>; Candida tropicalis, gel filtration, sedimentation equilibrium centrifugation <26>; pig kidney, gel filtration <32, 35>; rabbit liver, gel filtration <39>) <23, 26, 32, 35, 39> -999 #5,13# (differences in MW partially due to method of solubilization) <9, 20>

Subunits	? #1-3,5,7,10,13,14# (x * 72000-87000, pig, SDS-PAGE <1, 11, 14, 29>; rabbit, SDS-PAGE <3>; horse, SDS-PAGE <5>; rat, SDS-PAGE <5, 10, 16, 27, 29>; hamster, SDS-PAGE <8>; Helianthus tuberosus, SDS-PAGE <9>; Lodderomyces elongisporus, SDS-PAGE <17>; Candida tropicalis, SDS-PAGE <20>; Spodoptera eridania, SDS-PAGE <21>) <1, 3, 5, 8-11, 14, 16, 17, 20, 21, 27, 29> Dimer #6,8,12# (2 * 36000, Nitrobacter winogradskyi, SDS-PAGE <7>; 2 * 52000, Trypanosoma cruzi, SDS-PAGE <12>; 2 * 34300-40000, Saccharomyces cerevisiae, SDS-PAGE, sedimentation equilibrium centrifugation after treatment with guanidine-HCl <23>) <7, 12, 23> Monomer #3,12# (72000, Saccharomyces cerevisiae, SDS-PAGE <28>; 75000, rabbit, Triton-solubilized, SDS-PAGE <39>; 68000, rabbit, trypsin-solubilized, SDS-PAGE <39>) <28, 39> More #5,13# (differences in subunit weight partially due to method of solubilization) <9, 20>
Temperature stability (deg.C)	100 #1# (10 min, inhibition of O2-formation) <14> 60 #2# (inactivation) <10> 40 #14# (50% activity) <21> 36 #14# (inactivation above) <21> 25-30 #2# (diluted solutions: gradual loss of activity) <41> -999 #12# (FAD and NADPH: protection against thermal inactivation) <23>
General stability	#12,13# FAD, FMN necessary for stabilization during purification <20, 28> #1# Instable during purification <32>

Storage stability

- #2# -15°C or-20°C, 10 mM phosphate buffer, pH 7.5, several months <41>
- #14# -15°C, more than 1 year <21>
- #3# -20°C, N2-atmosphere, several weeks <30>
- #13# -70°C, 0.15 mM potassium phosphate buffer, pH 7, 1 mM mercaptoethanol, 1 mM EDTA, 1 micromol FMN, 1 micromol FAD, 0.3% Mülgofen BC-720, 30% glycerol, several months <20>
- #2# -78°C, 30 mM potassium phosphate buffer, pH 7.7, 0.1 mM EDTA, 20% glycerol, 0.4 mM PMSF <16>
- #2# -80°C <10>
- #7# -80°C, 50 mM phosphate buffer, pH 7.4, 0.1 mM EDTA, 20% glycerol <8>
- #8# -90°C or-20°C, 24 h, 5-10% loss of activity, reactivation by FAD <12>
- #14# 0-4°C, several months <21>
- #2# 0°C, some days <41>
- #2# 4°C or room temperature, FAD-depleted enzyme <2>

Renaturated

#1,3,5# (reconstitution of O2- generating system, #3# <3>; reconstitution of monooxygenase system, #5# <9>) <3, 9, 30, 38>

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BRENDA:1.6.2.4_Aspergillus_ochraceus

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=> d

L1   ANSWER 1 OF 1  REGISTRY  COPYRIGHT 2001 ACS
RN   9038-14-6  REGISTRY
CN   Oxygenase, mono- (9CI)  (CA INDEX NAME)
OTHER NAMES:
CN   Baeyer-Villigerase
CN   Cytochrome P 450 hydroperoxidase
CN   Cytochrome P 450 monooxygenase
CN   Cytochrome P 450-linked monooxygenase
CN   Cytochrome P-450 mixed-function oxidase
CN   E.C. 1.14.14.1
CN   E.C. 1.14.14.2
CN   Flavin monooxygenase
CN   Flavin-containing monooxygenase
CN   Flavin-contg. monooxygenase
CN   Flavin-contg. monooxygenase 1
CN   Flavin-contg. monooxygenase 3
CN   Flavoprotein monooxygenase
CN   Flavoprotein-linked monooxygenase
CN   HCE hydroxylase
CN   Microsomal monooxygenase
CN   Mixed function monooxygenase
CN   Mixed-function oxidase
CN   Mixed-function oxygenase
CN   Monooxygenase
CN   Oxidase, mixed function
CN   Oxygenase, flavoprotein-linked mono-
DR   9040-60-2, 55963-41-2, 62213-32-5
MF   Unspecified
CI   MAN
LC   STN Files:   AGRICOLA, ANABSTR, BIOBUSINESS, BIOSIS, BIOTECHNO, CA,
       CAPLUS, CASREACT, CEN, CIN, CSNB, EMBASE, IFICDB, IFIPAT, IFIUDB, PIRA,
       PROMT, TOXLINE, TOXLIT, ULIDAT, USPATFULL

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
              3903 REFERENCES IN FILE CA (1967 TO DATE)
                22 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA
              3913 REFERENCES IN FILE CAPLUS (1967 TO DATE)
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BRENDA:1.14.14.1

E.C. number	1.14.14.1 (BRENDA copyright notice)
Original Organism	#1# Mammals (e.g. mouse <1, 2>; rabbit <3>. There is no clear evidence whether the enzymes isolated from microsomes of different species, or even from the same species by different research groups are identical) <1-3>
Systematic name	Substrate,reduced-flavoprotein:oxygen oxidoreductase (RH-hydroxylating or-epoxidizing)
Recommended name	Unspecific monooxygenase
Synonyms	Microsomal monooxygenase EC 1.99.1.1 (formerly) EC 1.14.99.8 (formerly) EC 1.14.1.1 (formerly) Microsomal P-450 Aryl hydrocarbon hydroxylase Aryl-4-monooxygenase Xenobiotic monooxygenase Flavoprotein-linked monooxygenase Flavoprotein monooxygenase Oxygenase, flavoprotein-linked mono- EC 1.14.14.2 (formerly)
CAS registration number	62213-32-5
Reaction	RH + reduced flavoprotein + O2 = ROH + oxidized flavoprotein + H2O
Reaction type	Deamination Desulfation Epoxidation Hydroxylation N-, S-, O-Dealkylation N-Oxidation Redox reaction Reduction of azo, nitro, N-oxide groups Sulfoxidation

Substrates/products	S: Aryl hydrocarbons + reduced flavoprotein + O2 #1# (e.g. benzo[a]pyrene, ethoxyresuforin, biphenyl, p-nitroanisole, acetanilide, 2-acetylaminofluorene, 2-ethoxycoumarin, estradiol-17beta, testosterone, #1# <1, 2>; prostaglandins, #1# <3>) <1-3> P: ? S: More #1# (acts on a wide range of substrates including many xenobiotics, steroids, fatty acids, vitamins and prostaglandins. Depending on the procedure of induction and chromatography numerous forms of enzyme can be isolated. Up to now there is no clear evidence whether a special form of P-450 exists for each of the different reaction types, or several nonspecific enzymes catalyze more than 1 reaction. The enzymes from different organisms and from different tissues of a single organism are not comparable, those described in, #1# <1-3> display only a small part of a wide spectrum of possible reactions) <1-3> P: ?
Source tissue	Liver #1# <1-3>
Localisation	Microsomes #1# (16 different cytochrome P-450 have been isolated from mouse liver of which each contains numerous different forms of P-450) <1, 2>
References	<1> Lang, M.A., Nebert, D.W.: Structural gene products of the Ah locus. Evidence for many unique P-450-mediated monooxygenase activities reconstituted from 3-methylcholanthrene-treated C57BL/6N mouse liver microsomes:: J. Biol. Chem., 256; 12058-12067 (1981) <2> Lang, M.A., Gielen, J.E., Nebert, D.W.: Genetic evidence for many unique liver microsomal P-450-mediated monooxygenase activities in heterogeneic stock mice:: J. Biol. Chem., 256; 12068-12075 (1981) <3> Theoharides, A.D., Kupfer, D.: Evidence for different hepatic microsomal monooxygenases catalyzing omega- and (omega-1)-hydroxylations of prostaglandins E1 and E2. Effects of inducers of monooxygenase on the kinetic constants of prostaglandin hydroxylation:: J. Biol. Chem., 256; 2168-2175 (1981)

BRENDA:1.14.14.1_Mammals

E.C. number	1.14.14.1 (BRENDA copyright notice)
Original Organism	Mammals (e.g. mouse <1,2>; rabbit <3>; . There is no clear evidence whether the enzymes isolated from microsomes of different species, or even from the same species by different research groups are identical) <1-3>

Substrates/products

S: Aryl hydrocarbons + reduced flavoprotein + O_2 (e.g. benzo[a]pyrene, ethoxyresuforin, biphenyl, p-nitroanisole, acetanilide, 2-acetylaminofluorene, 2-ethoxycoumarin, estradiol-17beta, testosterone <1,2>; prostaglandins <3>) <1-3>

P: ?

S: More (acts on a wide range of substrates including many xenobiotics, steroids, fatty acids, vitamins and prostaglandins. Depending on the procedure of induction and chromatography numerous forms of enzyme can be isolated. Up to now there is no clear evidence whether a special form of P-450 exists for each of the different reaction types, or several nonspecific enzymes catalyze more than 1 reaction. The enzymes from different organisms and from different tissues of a single organism are not comparable, those described in <1,2,3>; display only a small part of a wide spectrum of possible reactions) <1-3>

P: ?

Source tissue

Liver <1-3>

Localisation

Microsomes (16 different cytochrome P-450 have been isolated from mouse liver of which each contains numerous different forms of P-450) <1, 2>

References

<1> Lang, M.A., Nebert, D.W.: Structural gene products of the Ah locus. Evidence for many unique P-450-mediated monooxygenase activities reconstituted from 3-methylcholanthrene-treated C57BL/6N mouse liver microsomes:: J. Biol. Chem., 256; 12058-12067 (1981)

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Systematic name	Substrate,reduced-flavoprotein:oxygen oxidoreductase (RH-hydroxylating or-epoxidizing)
Recommended name	Unspecific monooxygenase
Synonyms	Microsomal monooxygenase EC 1.99.1.1 (formerly) EC 1.14.99.8 (formerly) EC 1.14.1.1 (formerly) Microsomal P-450 Aryl hydrocarbon hydroxylase Aryl-4-monooxygenase Xenobiotic monooxygenase Flavoprotein-linked monooxygenase Flavoprotein monooxygenase Oxygenase, flavoprotein-linked mono- EC 1.14.14.2 (formerly)
CAS registration number	62213-32-5
Reaction	RH + reduced flavoprotein + O2 = ROH + oxidized flavoprotein + H2O
Reaction type	Deamination Desulfation Epoxidation Hydroxylation N-, S-, O-Dealkylation N-Oxidation Redox reaction Reduction of azo, nitro, N-oxide groups Sulfoxidation

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NiceZyme View of ENZYME: EC 1.14.14.1

Official Name

Unspecific monooxygenase.

Alternative Name(s)

Microsomal monooxygenase.
Xenobiotic monooxygenase.
Aryl-4-monooxygenase.
Aryl hydrocarbon hydroxylase.
Microsomal p450.
Flavoprotein-linked monooxygenase.
Cytochrome p450.

Reaction catalysed

```
    RH
 +  reduced flavoprotein
 +  O(2)
<=>
    ROH
 +  oxidized flavoprotein
 +  H(2)O
```

Cofactor(s)

Heme-thiolate.

Comments

- Acts on a wide range of substrates including many xenobiotics, steroids, fatty acids, vitamins and prostaglandins.
- Reactions catalysed include hydroxylation, epoxidation, N-oxidation, sulfooxidation, N-, S- and O-dealkylations, desulfation, deamination, and reduction of azo, nitro, and N-oxide groups.

Cross-References

Biochemical Pathways; map number(s)	T6, U6
PROSITE	PDOC00081
BRENDA	1.14.14.1
EMP/PUMA	1.14.14.1

WIT	1.14.14.1
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	P33264,	CPCR_MESAU;	P33265,	CPCS_MESAU;	Q64458,	CPCT_MOUSE;
	Q29510,	CPCU_RABIT;	Q29478,	CPCV_CAPAE;	P10633,	CPD1_RAT ;
	P10634,	CPD2_RAT ;	P12938,	CPD3_RAT ;	P13108,	CPD4_RAT ;
	P12939,	CPD5_RAT ;	P10635,	CPD6_HUMAN;	P11714,	CPD9_MOUSE;
	P24456,	CPDA_MOUSE;	P24457,	CPDB_MOUSE;	Q01361,	CPDE_BOVIN;
	Q29473,	CPDF_CANFA;	Q64403,	CPDG_CAVPO;	Q29488,	CPDH_MACFA;
	Q64680,	CPDI_RAT ;	O18992,	CPDJ_CALJA;	O18963,	CPE1_BOVIN;
	P05181,	CPE1_HUMAN;	P33266,	CPE1_MACFA;	P51581,	CPE1_MESAU;
	Q05421,	CPE1_MOUSE;	P79383,	CPE1_PIG ;	P08682,	CPE1_RABIT;
	P05182,	CPE1_RAT ;	P33274,	CPF1_RAT ;	P51869,	CPF4_RAT ;
	P51870,	CPF5_RAT ;	P51871,	CPF6_RAT ;	P24461,	CPG1_RABIT;
	P10610,	CPG1_RAT ;	P05180,	CPH1_CHICK;	P20678,	CPH2_CHICK;
	P52786,	CPJ1_RABIT;	P51589,	CPJ2_HUMAN;	P51590,	CPJ3_RAT ;
	O54749,	CPJ5_MOUSE;	O54750,	CPJ6_MOUSE;	Q92090,	CPK1_ONCMY;
	O93299,	CPK3_ONCMY;	O93297,	CPK4_ONCMY;	Q27712,	CPL1_PANAR;
	Q92088,	CPM1_ONCMY;	P46194,	CPV1_BOVIN;	O42145,	CPV1_BRARE;
	P79690,	CPV1_CARAU;	P19098,	CPV1_CHICK;	P79699,	CPV1_COTJA;
	O46512,	CPV1_HORSE;	P11511,	CPV1_HUMAN;	Q92111,	CPV1_ICTPU;
	P28649,	CPV1_MOUSE;	P70091,	CPV1_ORENI;	Q92087,	CPV1_ORYLA;
	Q29624,	CPV1_PIG ;	Q92112,	CPV1_POEGU;	Q29605,	CPV1_RABIT;
	P22443,	CPV1_RAT ;	Q9XS28,	CPV1_SHEEP;	O73686,	CPV2_CARAU;
	P79430,	CPV2_PIG ;	P79304,	CPV3_PIG ;	P14779,	CPXB_BACME;
	P14762,	CPXI_BACME;	P56654,	CPZ2_MOUSE;	P56655,	CPZ3_MOUSE;
	P56656,	CPZ4_MOUSE;	P56657,	CPZ5_MOUSE;	O62671,	CPZ6_CANFA;
	P79402,	CPZ7_PIG ;				

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BRENDA:1.3.3.6

E.C. number	1.3.3.6 (BRENDA copyright notice)
Original Organism	#1# Spinacia oleracea (spinach) <20> #2# Vigna radiata (mung bean) <20> #3# Phanerochaete chrysosporium <21> #4# Cucumis sativus (cucumber) <22> #5# Candida tropicalis (pK 233) <1, 13-16> #6# Rat (3 forms: 1. inducible fatty acyl-CoA oxidase, 2. noninducible fatty acyl-CoA oxidase, 3. noninducible trihydroxycoprostanoyl-CoA oxidase <11>) <2-4, 6-11> #7# Candida lipolytica <5> #8# Candida maltosa <18> #9# Human <12> #10# Saccharomyces cerevisiae <17> #11# Mouse <19>
Systematic name	Acyl-CoA:oxygen 2-oxidoreductase
Recommended name	Acyl-CoA oxidase
Synonyms	Oxidase, acyl-coenzyme A Fatty acyl-CoA oxidase Acyl coenzyme A oxidase Fatty acyl-coenzyme A oxidase
CAS registration number	61116-22-1
Reaction	Acyl-CoA + O2 = trans-2,3-dehydroacyl-CoA + H2O2 (acts on CoA derivatives of fatty acids with chain length from 8 to 18)
Reaction type	More #7# (anti-elimination of pro-2R and pro-3R hydrogens of acyl-CoA) <5> Redox reaction
Substrates/products	S: Lauroyl-CoA + O2 #1,2,5,6# <6, 13, 15, 20> P: trans-2-Dodecenoyl-CoA + H2O2 S: Arachidoyl-CoA + O2 #5# <13> P: trans-2,3-Dehydro-5,8,11,14-eicosatetraenoyl-CoA + H2O2 S: Dec-4-cis-enoyl-CoA + O2 #6# <3> P: ? S: 2-Oxoheptadecyldethio-CoA + O2 #5# <14>

[redacted]

P: ?

S: Dicarboxylic acid-CoAs with 6-16 carbon atoms + O2 #6# <10>

P: ?

S: Butyryl-CoA + O2 #1,2# (not, #3,6# <9, 21>) <20>

P: trans-2-Butenoyl-CoA + H2O2

S: Linoleoyl-CoA + O2 #1,2,6# <6, 20>

P: trans-2,3-Dehydro-9,12-octadienoyl-CoA + H2O2

S: Oleoyl-CoA + O2 #5,6# <6, 13>

P: trans-2,3-Dehydro-9-octadecenoyl-CoA + H2O2

S: Myristoyl-CoA + O2 #1,2,5,6# <6, 13, 20>

P: trans-2-Tetradecenoyl-CoA + H2O2

S: Octanoyl-CoA + O2 #1,2,5,6# <6, 13, 20>

P: trans-2-Octenoyl-CoA + H2O2

S: Leuko-dichlorofluorescein + O2 #6# <7>

P: ?

S: Nonanoyl-CoA + O2 #7# <5>

P: trans-2-Nonenoyl-CoA + H2O2

S: Stearoyl-CoA + O2 #1,5-7# <5, 6, 13, 20>

P: trans-2-Octadecenoyl-CoA + H2O2

S: Hexadecanedioyl-CoA + O2 #6# <4>

P: ?

S: Palmitoyl-CoA + O2 #1,2,5,6# <4, 6, 7, 9, 13, 20>

P: trans-2,3-Dehydrohexadecanoyl-CoA + H2O2 (trans-2-hexadecenoyl-CoA)

S: Acyl-CoA + O2 #1-7# (specificity: C4-C20 acyl-CoA, #5# <13>; C8-C18 acyl CoA, #3# <21>; most active towards C12-C18 acyl-CoA, C20 and C22 acyl-CoA also oxidized, C4 and C6 acyl-CoA hardly oxidized, #6# <9>; C4-C18 monocarboxylic acid-CoA, #6# <10>; C6-C16 dicarboxylic-CoA, #6# <10>; 3'-phosphate on the ribose ring and the structure of the adenine moiety are essential for substrate recognition, specificity is relatively low with respect to the structure of the pantonic acid moiety, #6# <6>; chain-length specificity changes with acyl-CoA concentration used, #6# <7>; Cucumis sativus: enzyme acts selectively on fatty acyl-CoA with 16 or 18 carbon atoms, cis-9-unsaturated esters with a C16 or C18 acyl moiety being converted with higher rate than saturated or polyunsaturated fatty acyl-CoA, #4# <22>; anti-elimination of pro-2R and pro-3R hydrogens of acyl-CoA, #7# <5>) <3-9, 10, 13-15, 20-22>

	P: trans-2,3-Dehydroacyl-CoA + H2O2 S: Trihydroxycoprostanoyl-CoA + O2 #6# <4> P: ? S: Decanoyl-CoA + O2 #5,6# <6, 13> P: trans-2-Decenoyl-CoA + H2O2
Natural substrates	Acyl-CoA + O2 #5,6,9# (CoA derivatives of fatty acids with chain length from 8 to 18, first reaction of peroxisomal beta-oxidation, rate limiting for this process, #6,9# <7, 8, 12>; beta-oxidation of dicarboxylic acid-CoAs in rat liver is carried out exclusively in peroxisomes, #6# <10>; significance in metabolism of alkanes of Candida tropicalis, #5# <16>) <7, 8, 10, 12, 16>
Turnover number (1/min)	-999 #5# (pH-dependency of turnover number) <15>
Specific activity (micromol/min/mg)	27.2 #6# <8> 19.13 #5# <13> 2.04 #6# <6> 1.45 #6# <9> -999 #5# <14>
Km-value (mM)	0.087 #6# {octanoyl-CoA} (liver enzyme) <7> 0.058 #6# {octanoyl-CoA} <6> 0.046 #5# {oleoyl-CoA} <13> 0.042 #5# {octanoyl-CoA} <13> 0.034 #5# {stearoyl-CoA} <13> 0.0335 #5# {arachidoyl-CoA} <13> 0.032 #1# {butyryl-CoA} <20> 0.029 #5# {myristoyl-CoA} <13> 0.027 #6# {lauroyl-CoA} (liver enzyme) <6> 0.025 #5# {dodecanoyl-CoA} (pH 7-9.5) <15> 0.024 #5# {decanoyl-CoA} (lauroyl-CoA) <13> 0.023 #1# {stearoyl-CoA} <20> 0.02 #6# {decanoyl-CoA} <6> 0.019 #1# {linoleoyl-CoA} <20> 0.013 #6# {lauroyl-CoA} <6> 0.0116 #6# {myristoyl-CoA} (palmitoyl-CoA) <6> 0.011 #1,6# {myristoyl-CoA} (#1# <20>; oleoyl CoA, #6# <6>) <6, 20> 0.0096 #6# {stearoyl-CoA} <6>

	0.0093 #6# {dec-4-cis-enoyl-CoA} <3> 0.0073 #6# {linoleoyl-CoA} <6> 0.007 #6# {palmitoyl-CoA} (liver enzyme) <7> 0.005 #6# {O2} <6> 0.00181 #6# {palmitoyl-CoA} (kidney enzyme) <7>
pH-optimum	8 #5,6# <6, 13>
pH-range	7-10 #6# (7: about 30% of activity maximum, 10: about 5% of activity maximum, inactive below pH 6.5) <6>
Temperature-optimum (deg.C)	50 #5# <13>
Cofactors/prosthetic groups	FAD #5,6# (flavoprotein, #5,6# <6, 7, 13-15>; prosthetic group, #6# <6>; 1.22 mol per mol of enzyme, #6# <6>; flavoprotein with noncovalently bound FAD, #6# <7>; 8 mol FAD per mol of enzyme, 1 mol FAD per mol of subunit, #5# <13, 14>) <6, 7, 13-15>
Inhibitors	3-Ketohexadecanoyl-CoA #6# <6> Acetyl-CoA #6# <3> AgNO3 #5# <13> Antimycin A #6# <4> C16-C18 fatty acyl-CoA #11# (at fairly low concentrations) <19> CH3COOK #6# <6> CoA #6# <3> FMN #6# <3> HgCl2 #5# <13> KBr #6# <6> KCl #6# <6> KI #6# <6> KNO3 #6# <6> Mercuric acetate #5# <13> NaCl #6# <6> NaN3 #6# <6> NH4Cl #6# <6> NH4SCN #6# <6> p-Chloromercuribenzoate #5# <13>

Source tissue	Adrenal gland #6# <7> Heart #6# <7> Kidney #6,11# <7, 19> Liver #6,9# <3, 6-12> Mycelium #3# <21> Seedlings #4# (cotyledons) <22> Skeletal muscle #6# <7>
Localisation	Extracellular #3# <21> Glyoxysomes #4# <22> Peroxisomes #1,2,5,6,9,10# <4, 6, 8, 10-12, 15-17, 20>
Purification	#4# (cucumber) <22> #5# <13, 15> #6# <6, 8, 9>
Crystallisation	#5# <13>
Molecular Weight	600000 #5# (Candida tropicalis, sedimentation equilibrium) <13> 552000 #5# (Candida tropicalis, ultracentrifugation) <15> 427000 #6# (rat liver, noninducible fatty acyl-CoA oxidase, gel filtration) <11> 150000 #4# (Cucumis sativus, gel filtration) <22> 145000 #6# (rat liver, inducible fatty acyl-CoA oxidase, gel filtration) <11> 139000 #6# (rat liver, sedimentation equilibrium method <6>; noninducible trihydroxycoprostanoyl-CoA oxidase <11>) <6, 11>
Subunits	Dimer #4,6# (2 * 71000, rat liver, SDS-PAGE, noninducible fatty acyl-CoA oxidase <11>; 2 * 72000, Cucumis sativus, SDS-PAGE <22>) <11, 22> Hexamer #6# (6 * 69000, rat liver, SDS-PAGE, noninducible trihydroxyprostanoyl-CoA oxidase) <11> Octamer #5# (8 * 74000 <13>; 8 * 75000 <14>; Candida tropicalis, SDS-PAGE <13, 14>) <13, 14> Oligomer #5,6# (x * 72100, Candida tropicalis, SDS-PAGE <15>; x * 52000, x * 22500, rat liver, SDS-PAGE, inducible fatty acyl-CoA oxidase <11>) <11, 15> Tetramer #6# (2 * 45000 + 2 * 22000, rat, SDS-PAGE) <8>
Cloned	#5,6# (Candida tropicalis pK 233 <1>; rat <2>) <1, 2>
pH-stability	5.5-9 #5# (35°C, 60 min) <13>

Temperature stability (deg.C)	65 #5# (10 min, complete inactivation) <13> 50 #5# (10 min) <13>
General stability	#4# Dialysis, 4°C, 24 h, 80% loss of activity <22>
Storage stability	#5# -20°C, 25% glycerol, 8 months <15> #6# -20°C, for at least 1 month <6> #5# -20°C, pH 7.4, 2 months <14> #5# 4°C, pH 7.4, 2 months, 20% loss of activity <14> #4# Frozen, 10% sucrose, several weeks <22>

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